

SEQUENCE LISTING

<110> Meyers, Rachel

<120> 21612, 21615, 21620, 21676, 33756, Novel
Human Alcohol Dehydrogenases

<130> 5800-49

<160> 10

<170> FastSEQ for Windows Version 3.0

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<211> 260

<212> PRT

<213> Homo sapiens

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35 40 45
Glu Glu Leu Ala Ala Glu Cys Lys Ser Ala Gly Tyr Pro Gly Thr Leu
50 55 60
Ile Pro Tyr Arg Cys Asp Leu Ser Asn Glu Glu Asp Ile Leu Ser Met
65 70 75 80
Phe Ser Ala Ile Arg Ser Gln His Ser Gly Val Asp Ile Cys Ile Asn
85 90 95
Asn Ala Gly Leu Ala Arg Pro Asp Thr Leu Leu Ser Gly Ser Thr Ser
100 105 110
Gly Trp Lys Asp Met Phe Asn Val Asn Val Leu Ala Leu Ser Ile Cys
115 120 125
Thr Arg Glu Ala Tyr Gln Ser Met Lys Glu Arg Asn Val Asp Asp Gly
130 135 140
His Ile Ile Asn Ile Asn Ser Met Ser Gly His Arg Val Leu Pro Leu
145 150 155 160
Ser Val Thr His Phe Tyr Ser Ala Thr Lys Tyr Ala Val Thr Ala Leu
165 170 175
Thr Glu Gly Leu Arg Gln Glu Leu Arg Glu Ala Gln Thr His Ile Arg
180 185 190
Ala Thr Cys Ile Ser Pro Gly Val Val Glu Thr Gln Phe Ala Phe Lys
195 200 205
Leu His Asp Lys Asp Pro Glu Lys Ala Ala Ala Thr Tyr Glu Gln Met
210 215 220
Lys Cys Leu Lys Pro Glu Asp Val Ala Glu Ala Val Ile Tyr Val Leu
225 230 235 240
Ser Thr Pro Ala His Ile Gln Ile Gly Asp Ile Gln Met Arg Pro Thr
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Glu Gln Val Thr
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 <213> Homo sapiens

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<221> CDS
 <222> (421)...(1203)

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aagaactgct	cctcagtgag	tgttgccttt	acttctaggc	ctgtacggaa	gtgttacttc	240
tgctctaaaa	gctgcggaat	tctaatacga	ctcactatag	ggagtcgacc	cacgcgtccg	300
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atg gcc agg ccc ggc atg gag cgg tgg cgc gac	cgg ctg gcg ctg gtg	468				
Met Ala Arg Pro Gly Met Glu Arg Trp Arg Asp Arg Leu Ala Leu Val						
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acg ggg gcc tcg ggg ggc atc ggc gcg gcc gtg gcc cgg gcc ctg gtc	516					
Thr Gly Ala Ser Gly Gly Ile Gly Ala Ala Val Ala Arg Ala Leu Val						
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Gln Gln Gly Leu Lys Val Val Gly Cys Ala Arg Thr Val Gly Asn Ile						
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gag gag ctg gct gct gaa tgt aag agt gca ggc tac ccc ggg act ttg	612					
Glu Glu Leu Ala Ala Glu Cys Lys Ser Ala Gly Tyr Pro Gly Thr Leu						
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Ile Pro Tyr Arg Cys Asp Leu Ser Asn Glu Glu Asp Ile Leu Ser Met						
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Phe Ser Ala Ile Arg Ser Gln His Ser Gly Val Asp Ile Cys Ile Asn						
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aat gct ggc ttg gcc cgg cct gac acc ctg ctc tca ggc agc acc agt	756					
Asn Ala Gly Leu Ala Arg Pro Asp Thr Leu Leu Ser Gly Ser Thr Ser						
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Gly Trp Lys Asp Met Phe Asn Val Asn Val Leu Ala Leu Ser Ile Cys						
115 120 125						
aca cgg gaa gcc tac cag tcc atg aag gag cgg aat gtg gac gat ggg	852					

Thr	Arg	Glu	Ala	Tyr	Gln	Ser	Met	Lys	Glu	Arg	Asn	Val	Asp	Asp	Gly	
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cac	atc	att	aac	atc	aat	agc	atg	tct	ggc	cac	cga	gtg	tta	ccc	ctg	900
His	Ile	Ile	Asn	Ile	Asn	Ser	Met	Ser	Gly	His	Arg	Val	Leu	Pro	Leu	
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Ser	Val	Thr	His	Phe	Tyr	Ser	Ala	Thr	Lys	Tyr	Ala	Val	Thr	Ala	Leu	
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Thr	Glu	Gly	Leu	Arg	Gln	Glu	Leu	Arg	Glu	Ala	Gln	Thr	His	Ile	Arg	
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gcc	acg	tgc	atc	tct	cca	ggt	gtg	gtg	gag	aca	caa	ttc	gcc	ttc	aaa	1044
Ala	Thr	Cys	Ile	Ser	Pro	Gly	Val	Val	Glu	Thr	Gln	Phe	Ala	Phe	Lys	
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ctc	cac	gac	aag	gac	cct	gag	aag	gca	gct	gcc	acc	tat	gag	caa	atg	1092
Leu	His	Asp	Lys	Asp	Pro	Glu	Lys	Ala	Ala	Ala	Thr	Tyr	Glu	Gln	Met	
	210					215					220					
aag	tgt	ctc	aaa	ccc	gag	gat	gtg	gcc	gag	gct	gtt	atc	tac	gtc	ctc	1140
Lys	Cys	Leu	Lys	Pro	Glu	Asp	Val	Ala	Glu	Ala	Val	Ile	Tyr	Val	Leu	
225					230				235						240	
agc	act	ccc	gca	cac	atc	cag	att	gga	gac	atc	cag	atg	agg	ccc	acg	1188
Ser	Thr	Pro	Ala	His	Ile	Gln	Ile	Gly	Asp	Ile	Gln	Met	Arg	Pro	Thr	
				245				250						255		
gag	cag	gtg	acc	tag	tgactgtggg	agctcctcct	tcctcccca	cccttcatgg								1243
Glu	Gln	Val	Thr	*												
			260													
cttgccctcct	gcctctggat	tttaggtggt	gatttctgga	tcacgggata	ccacttccctg											1303
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tgcttcagtt	gtaaatgtga	aaaatgggct	ggggaaagga	ggtgggtgtcc	ctaattgttt											1423
tacttggttaa	cttggtcttg	tgccctggg	cacttggcct	ttgtctgctc	tcagtgtctt											1483
ccctttgaca	tgggaaagga	gttggtggcca	aaatccccat	cttcttgcac	ctcaacgtct											1543
gtggctyang	ggctgggggtg	gcagagggag	gccttcacct	tatatctgtg	ttgttatcca											1603
gggctccaga	cttctctctc	tgctgcccc	actgcaccct	ctccccctta	tctatctcct											1663
tctcggtctc	ccagcccagt	cttggtctct	tgtccccctc	tgggggtcatc	cctccactct											1723
gactctgact	atggcagcag	aacaccaggg	cctggcccag	tggatttcat	ggtgatcatt											1783
aaaaaaagaaa	aatcgcaacc	aaaaaaaaaaa	aaaaaagggc	gggccgctag	actagtytag											1843
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 <213> Homo sapiens

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Ile Leu Ile Asn Asn Ala Gly Val Met Arg Cys Pro His Trp Thr Thr	50	55	60		
Glu Asp Gly Phe Glu Met Gln Phe Gly Val Asn His Leu Gly His Phe	65	70	75	80	
Leu Leu Thr Asn Leu Leu Leu Asp Lys Leu Lys Ala Ser Ala Pro Ser	85	90	95		
Arg Ile Ile Asn Leu Ser Ser Leu Ala His Val Ala Gly His Ile Asp	100	105	110		
Phe Asp Asp Leu Asn Trp Gln Thr Arg Lys Tyr Asn Thr Lys Ala Ala	115	120	125		
Tyr Cys Gln Ser Lys Leu Ala Ile Val Leu Phe Thr Lys Glu Leu Ser	130	135	140		
Arg Arg Leu Gln Gly Ser Gly Val Thr Val Asn Ala Leu His Pro Gly	145	150	155	160	
Val Ala Arg Thr Glu Leu Gly Arg His Thr Gly Ile His Gly Ser Thr	165	170	175		
Phe Ser Ser Thr Thr Leu Gly Pro Ile Phe Trp Leu Leu Val Lys Ser	180	185	190		
Pro Glu Leu Ala Ala Gln Pro Ser Thr Tyr Leu Ala Val Ala Glu Glu	195	200	205		
Leu Ala Asp Val Ser Gly Lys Tyr Phe Asp Gly Leu Lys Gln Lys Ala	210	215	220		
Pro Ala Pro Glu Ala Glu Asp Glu Glu Val Ala Arg Arg Leu Trp Ala	225	230	235	240	
Glu Ser Ala Arg Leu Val Gly Leu Glu Ala Pro Ser Val Arg Glu Gln	245	250	255		
Pro Leu Pro Arg	260				

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 <213> Homo sapiens

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 <223> 33756 ADH

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gcaagctccg	cgccgacccc	tgacgcctga	cgctgtccc	cggcccgga	tgagccgcta	180
cctgtctccg	ctgtcggcgc	tgggcacggt	agcaggcgct	cgccgtgctg	ctcaagaggc	240
aacatcatcc	tggcctgccg	agac atg	gag aag	tgt gag	gcg gca	291
		Met	Glu	Lys	Cys	
			Glu	Ala	Ala	

gac atc cgc ggg gag acc ctc aat cac cat gtc aac gcc cgg cac ctg	339
Asp Ile Arg Gly Glu Thr Leu Asn His His Val Asn Ala Arg His Leu	
10 15 20 25	
gac ttg gct tcc ctc aag tct atc cga gag ttt gca gca aag atc att	387
Asp Leu Ala Ser Leu Lys Ser Ile Arg Glu Phe Ala Ala Lys Ile Ile	
30 35 40	
gaa gag gag gag cga gtg gac att cta atc aac aac gcg ggt gtg atg	435
Glu Glu Glu Glu Arg Val Asp Ile Leu Ile Asn Asn Ala Gly Val Met	
45 50 55	
cgg tgc ccc cac tgg acc acc gag gac ggc ttc gag atg cag ttt ggc	483
Arg Cys Pro His Trp Thr Thr Glu Asp Gly Phe Glu Met Gln Phe Gly	
60 65 70	
gtt aac cac ctg ggt cac ttt ctc ttg aca aac ttg ctg ctg gac aag	531
Val Asn His Leu Gly His Phe Leu Leu Thr Asn Leu Leu Leu Asp Lys	
75 80 85	
ctg aaag gcc tca gcc cct tcg cgg atc atc aac ctc tcg tcc ctg gcc	579
Leu Lys Ala Ser Ala Pro Ser Arg Ile Ile Asn Leu Ser Ser Leu Ala	
90 95 100 105	
cat gtt gct ggg cac ata gac ttt gac gac ttg aac tgg cag acg agg	627
His Val Ala Gly His Ile Asp Phe Asp Asp Leu Asn Trp Gln Thr Arg	
110 115 120	
aag tat aac acc aaa gcc gcc tac tgc cag agc aag ctc gcc atc gtc	675
Lys Tyr Asn Thr Lys Ala Ala Tyr Cys Gln Ser Lys Leu Ala Ile Val	
125 130 135	
ctc ttc acc aag gag ttg agc cgg cgg ctg caa ggc tct ggt gtg act	723
Leu Phe Thr Lys Glu Leu Ser Arg Arg Leu Gln Gly Ser Gly Val Thr	
140 145 150	
gtc aac gcc ctg cac ccc ggc gtg gcc agg aca gag ctg ggc aga cac	771
Val Asn Ala Leu His Pro Gly Val Ala Arg Thr Glu Leu Gly Arg His	
155 160 165	
acg ggc atc cat ggc tcc acc ttc tcc agc acc aca ctc ggg ccc atc	819
Thr Gly Ile His Gly Ser Thr Phe Ser Ser Thr Thr Leu Gly Pro Ile	
170 175 180 185	
ttc tgg ctg ctg gtc aag agc ccc gag ctg gcc gcc cag ccc agc aca	867
Phe Trp Leu Leu Val Lys Ser Pro Glu Leu Ala Ala Gln Pro Ser Thr	
190 195 200	
tac ctg gcc gtg gcg gag gaa ctg gcg gat gtt tcc gga aag tac ttc	915
Tyr Leu Ala Val Ala Glu Glu Leu Ala Asp Val Ser Gly Lys Tyr Phe	
205 210 215	
gat gga ctc aaa cag aag gcc ccg gcc ccc gag gct gag gat gag gag	963
Asp Gly Leu Lys Gln Lys Ala Pro Ala Pro Glu Ala Glu Asp Glu Glu	
220 225 230	

gtg gcc cgg agg ctt tgg gct gaa agt gcc cgc ctg gtg ggc tta gag 1011
 Val Ala Arg Arg Leu Trp Ala Glu Ser Ala Arg Leu Val Gly Leu Glu
 235 240 245

gct ccc tct gtg agg gag cag ccc ctc ccc aga taa cctctggagc 1057
 Ala Pro Ser Val Arg Glu Gln Pro Leu Pro Arg *
 250 255 260

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 ttcttggcac tacctgagcc gggagaccca ggactg 1153

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 <213> Homo sapiens

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 Lys Ala Thr Ile Pro Gly Lys Thr Val Ile Val Thr Gly Ala Asn Thr
 35 40 45
 Gly Ile Gly Lys Gln Thr Ala Leu Glu Leu Ala Arg Arg Gly Gly Asn
 50 55 60
 Ile Ile Leu Ala Cys Arg Asp Met Glu Lys Cys Glu Ala Ala Ala Lys
 65 70 75 80
 Asp Ile Arg Gly Glu Thr Leu Asn His His Val Asn Ala Arg His Leu
 85 90 95
 Asp Leu Ala Ser Leu Lys Ser Ile Arg Glu Phe Ala Ala Lys Ile Ile
 100 105 110
 Glu Glu Glu Glu Arg Val Asp Ile Leu Ile Asn Asn Ala Gly Val Met
 115 120 125
 Arg Cys Pro His Trp Thr Thr Glu Asp Gly Phe Glu Met Gln Phe Gly
 130 135 140
 Val Asn His Leu Gly His Phe Leu Leu Thr Asn Leu Leu Leu Asp Lys
 145 150 155 160
 Leu Lys Ala Ser Ala Pro Ser Arg Ile Ile Asn Leu Ser Ser Leu Ala
 165 170 175
 His Val Ala Gly His Ile Asp Phe Asp Asp Leu Asn Trp Gln Thr Arg
 180 185 190
 Lys Tyr Asn Thr Lys Ala Ala Tyr Cys Gln Ser Lys Leu Ala Ile Val
 195 200 205
 Leu Phe Thr Lys Glu Leu Ser Arg Arg Leu Gln Gly Ser Gly Val Thr
 210 215 220
 Val Asn Ala Leu His Pro Gly Val Ala Arg Thr Glu Leu Gly Arg His
 225 230 235 240
 Thr Gly Ile His Gly Ser Thr Phe Ser Ser Thr Thr Leu Gly Pro Ile
 245 250 255
 Phe Trp Leu Leu Val Lys Ser Pro Glu Leu Val Ala Gln Pro Ser Thr
 260 265 270
 Tyr Leu Ala Val Ala Glu Glu Leu Ala Asp Val Ser Gly Lys Tyr Phe
 275 280 285
 Asp Gly Leu Lys Gln Lys Ala Pro Ala Pro Glu Ala Glu Asp Glu Glu
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Ala Pro Ser Val Arg Glu Gln Pro Leu Pro Arg
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 <213> Homo sapiens
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 gctttttttt ttgggggncc cccccctttg ggaaccccn tggttttget tcaaacttct 180
 aaggcttttt gtttcgtttt ctgttcctgc gccgttacag atccaagytc tgaaaaacca 240
 gaaagttaac tggtaagttt agtccttttg tcttttattt cagggtcccgg atccggtggt 300
 ggtgcaaate aaagaactgc tcctcagtgg atgttgccct tactttctagg cctgtacgaa 360
 gtgttacttc tgctctaaaa gctgcggaat tctaatacga ctactatag ggagtcgacc 420
 cacgcgtccg cggacgcgtg ggcggacgcg tgggcggagc taccagggcg gctggtgtgc 480
 agcaagctcc gcgccgactc cggacgcctg acgcctgacg cctgtccccg gcccggc atg 540
 Met
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 agc cgc tac ctg ctg ccg ctg tcg gcg ctg ggc acg gta gca ggc gcc 588
 Ser Arg Tyr Leu Leu Pro Leu Ser Ala Leu Gly Thr Val Ala Gly Ala
 5 10 15
 gcc gtg ctg ctc aag gac tat gtc acc ggt ggg gct tgc ccc agc aag 636
 Ala Val Leu Leu Lys Asp Tyr Val Thr Gly Gly Ala Cys Pro Ser Lys
 20 25 30
 gcc acc atc cct ggg aag acg gtc atc gtg acg ggc gcc aac aca ggc 684
 Ala Thr Ile Pro Gly Lys Thr Val Ile Val Thr Gly Ala Asn Thr Gly
 35 40 45
 atc ggg aag cag acc gcc ttg gaa ctg gcc agg aga gga ggc aac atc 732
 Ile Gly Lys Gln Thr Ala Leu Glu Leu Ala Arg Arg Gly Gly Asn Ile
 50 55 60 65
 atc ctg gcc tgc cga gac atg gag aag tgt gag gcg gca gca aag gac 780
 Ile Leu Ala Cys Arg Asp Met Glu Lys Cys Glu Ala Ala Ala Lys Asp
 70 75 80
 atc cgc ggg gag acc ctc aat cac cat gtc aac gcc cgg cac ctg gac 828
 Ile Arg Gly Glu Thr Leu Asn His His Val Asn Ala Arg His Leu Asp
 85 90 95

ttg gct tcc ctc aag tct atc cga gag ttt gca gca aag atc att gaa	876
Leu Ala Ser Leu Lys Ser Ile Arg Glu Phe Ala Ala Lys Ile Ile Glu	
100 105 110	
gag gag gag cga gtg gac att cta atc aac aac gcg ggt gtg atg cgg	924
Glu Glu Glu Arg Val Asp Ile Leu Ile Asn Asn Ala Gly Val Met Arg	
115 120 125	
tgc ccc cac tgg acc acc gag gac ggc ttc gag atg cag ttt ggc gtt	972
Cys Pro His Trp Thr Thr Glu Asp Gly Phe Glu Met Gln Phe Gly Val	
130 135 140 145	
aac cac ctg ggt cac ttt ctc ttg aca aac ttg ctg ctg gac aag ctg	1020
Asn His Leu Gly His Phe Leu Leu Thr Asn Leu Leu Leu Asp Lys Leu	
150 155 160	
aaa gcc tca gcc cct tcg cgg atc atc aac ctc tcg tcc ctg gcc cat	1068
Lys Ala Ser Ala Pro Ser Arg Ile Ile Asn Leu Ser Ser Leu Ala His	
165 170 175	
gtt gct ggg cac ata gac ttt gac gac ttg aac tgg cag acg agg aag	1116
Val Ala Gly His Ile Asp Phe Asp Asp Leu Asn Trp Gln Thr Arg Lys	
180 185 190	
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Tyr Asn Thr Lys Ala Ala Tyr Cys Gln Ser Lys Leu Ala Ile Val Leu	
195 200 205	
ttc acc aag gag ctg agc cgg cgg ctg caa ggc tct ggt gtg act gtc	1212
Phe Thr Lys Glu Leu Ser Arg Arg Leu Gln Gly Ser Gly Val Thr Val	
210 215 220 225	
aac gcc ctg cac ccc ggc gtg gcc agg aca gag ctg ggc aga cac acg	1260
Asn Ala Leu His Pro Gly Val Ala Arg Thr Glu Leu Gly Arg His Thr	
230 235 240	
ggc atc cat ggc tcc acc ttc tcc agc acc aca ctc ggc ccc atc ttc	1308
Gly Ile His Gly Ser Thr Phe Ser Ser Thr Thr Leu Gly Pro Ile Phe	
245 250 255	
tgg ctg ctg gtc aag agc ccc gag ctg gtc gcc cag ccc agc aca tac	1356
Trp Leu Leu Val Lys Ser Pro Glu Leu Val Ala Gln Pro Ser Thr Tyr	
260 265 270	
ctg gcc gtg gcg gag gaa ctg gcg gat gtt tcc gga aag tac ttc gat	1404
Leu Ala Val Ala Glu Glu Leu Ala Asp Val Ser Gly Lys Tyr Phe Asp	
275 280 285	
gga ctc aaa cag aag gcc ccg gcc ccc gag gct gag gat gag gag gtg	1452
Gly Leu Lys Gln Lys Ala Pro Ala Pro Glu Ala Glu Asp Glu Glu Val	
290 295 300 305	
gcc cgg agg ctt tgg gct gaa agt gcc cgc ctg gtg ggc tta gag gct	1500
Ala Arg Arg Leu Trp Ala Glu Ser Ala Arg Leu Val Gly Leu Glu Ala	
310 315 320	
ccc tct gtg agg gag cag ccc ctc ccc aga taa cctctggagc agatttgaaa	1553

Pro Ser Val Arg Glu Gln Pro Leu Pro Arg *
 325 330

gccaggatgg cgcctccaga ccgaggacag ctgtccgcca tgcccgcagc ttcctggcac 1613
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<210> 7
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 <213> Homo sapiens

<400> 7

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Asp	Gly	Ala	Asn	Ile	Val	Ile	Ala	Ala	Lys	Thr	Ala	Gln	Pro	His	Pro
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Lys	Leu	Leu	Gly	Thr	Ile	Tyr	Thr	Ala	Ala	Glu	Glu	Ile	Glu	Ala	Val
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Gly	Gly	Lys	Ala	Leu	Pro	Cys	Ile	Val	Asp	Val	Arg	Asp	Glu	Gln	Gln
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Ile	Ser	Ala	Ala	Val	Glu	Lys	Ala	Ile	Lys	Lys	Phe	Gly	Gly	Ile	Asp
				85					90					95	
Ile	Leu	Val	Asn	Asn	Ala	Ser	Ala	Ile	Ser	Leu	Thr	Asn	Thr	Leu	Asp
			100					105					110		
Thr	Pro	Thr	Lys	Arg	Leu	Asp	Leu	Met	Met	Asn	Val	Asn	Thr	Arg	Gly
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Thr	Tyr	Leu	Ala	Ser	Lys	Ala	Cys	Ile	Pro	Tyr	Leu	Lys	Lys	Ser	Lys
		130				135					140				
Val	Ala	His	Ile	Leu	Asn	Ile	Ser	Pro	Pro	Leu	Asn	Leu	Asn	Pro	Val
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Trp	Phe	Lys	Gln	His	Cys	Ala	Tyr	Thr	Ile	Ala	Lys	Tyr	Gly	Met	Ser
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Met	Tyr	Val	Leu	Gly	Met	Ala	Glu	Glu	Phe	Lys	Gly	Glu	Ile	Ala	Val
			180				185						190		
Asn	Ala	Leu	Trp	Pro	Lys	Thr	Ala	Ile	His	Thr	Ala	Ala	Met	Asp	Met
		195					200					205			
Leu	Gly	Gly	Pro	Gly	Ile	Glu	Ser	Gln	Cys	Arg	Lys	Val	Asp	Ile	Ile
	210					215					220				
Ala	Asp	Ala	Ala	Tyr	Ser	Ile	Phe	Gln	Lys	Pro	Lys	Ser	Phe	Thr	Gly
225					230					235					240
Asn	Phe	Val	Ile	Asp	Glu	Asn	Ile	Leu	Lys	Glu	Glu	Gly	Ile	Glu	Asn
				245					250					255	
Phe	Asp	Val	Tyr	Ala	Ile	Lys	Pro	Gly	His	Pro	Leu	Gln	Pro	Asp	Phe
		260						265					270		
Phe	Leu	Asp	Glu	Tyr	Pro	Glu	Ala	Val	Ser	Lys	Lys	Val	Glu	Ser	Thr
		275					280						285		
Gly	Ala	Val	Pro	Glu	Phe	Lys	Glu	Glu	Lys	Leu	Gln	Leu	Gln	Pro	Lys
	290					295					300				
Pro	Arg	Ser	Gly	Ala	Val	Glu	Glu	Thr	Phe	Arg	Ile	Val	Lys	Asp	Ser
305					310					315					320
Leu	Ser	Asp	Asp	Val	Val	Lys	Ala	Thr	Gln	Ala	Ile	Tyr	Leu	Phe	Glu
				325					330					335	
Leu	Ser	Gly	Glu	Asp	Gly	Gly	Thr	Trp	Phe	Leu	Asp	Leu	Lys	Ser	Lys
			340					345					350		

Gly Gly Asn Val Gly Tyr Gly Glu Pro Ser Asp Gln Ala Asp Val Val
 355 360 365
 Met Ser Met Thr Thr Asp Asp Phe Val Lys Met Phe Ser Gly Lys Leu
 370 375 380
 Lys Pro Thr Met Ala Phe Met Ser Gly Lys Leu Lys Ile Lys Gly Asn
 385 390 395 400
 Met Ala Leu Ala Ile Lys Leu Glu Lys Leu Met Asn Gln Met Asn Ala
 405 410 415
 Arg Leu

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 tgactaattt tttttattta tgcagagccg aggcgcctc ggccctctgag ctattccaga 180
 agtagtgagg aggcctttttt ggaggcctag gcttttgcaa aaagctcctc gatcgagggg 240
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 gtcgcgttct gccgcctccc gcctgtggtg cctcctgaac tgcgtccgcc gtctaggtaa 360
 gtttaaagct cagggtcgaga ccgggccttt gtccggcgct cccttgaggc ctacctagac 420
 tcagccgggt ctccacgctt tgcttgacct tgcttgctca actctacgtc tttgtttcag 480
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 tttagtcttt ttgtctttta tttcagggtc cggatccggt ggtggtgcaa atcaaagaac 600
 tgctcctcag tggatgttgc ctttacttct aggcctgtac ggaagtgtta cttctgctct 660
 aaaagctgcg gaattctaata acgactcaat ataggwggtc gacccacgcg tccgctcgcc 720
 gccgcccgtg tcgccgccac ctctctctgat ctacgaaagt c atg tta ccc aac acc 776
 Met Leu Pro Asn Thr
 1 5
 ggg agg ctg gca gga tgt aca gtt ttt atc aca ggt gca agc cgt ggc 824
 Gly Arg Leu Ala Gly Cys Thr Val Phe Ile Thr Gly Ala Ser Arg Gly
 10 15 20
 att ggc aaa gct att gca ttg aaa gca gca aag gat gga gca aat att 872
 Ile Gly Lys Ala Ile Ala Leu Lys Ala Ala Lys Asp Gly Ala Asn Ile
 25 30 35
 gtt att gct gca aag acc gcc cag cca cat cca aaa ctt cta ggc aca 920
 Val Ile Ala Ala Lys Thr Ala Gln Pro His Pro Lys Leu Leu Gly Thr
 40 45 50

atc tat act gct gct gaa gaa att gaa gca gtt gga gga aag gcc ttg	968
Ile Tyr Thr Ala Ala Glu Glu Ile Glu Ala Val Gly Gly Lys Ala Leu	
55 60 65	
cca tgt att gtt gat gtg aga gat gaa cag cag atc agt gct gca gtg	1016
Pro Cys Ile Val Asp Val Arg Asp Glu Gln Gln Ile Ser Ala Ala Val	
70 75 80 85	
gag aaa gcc atc aag aaa ttt gga gga att gat att ctg gta aat aat	1064
Glu Lys Ala Ile Lys Lys Phe Gly Gly Ile Asp Ile Leu Val Asn Asn	
90 95 100	
gcc agt gcc att agt ttg acc aat aca ttg gac aca cct acc aag aga	1112
Ala Ser Ala Ile Ser Leu Thr Asn Thr Leu Asp Thr Pro Thr Lys Arg	
105 110 115	
ttg gat ctg atg atg aac gtg aac acc aga ggc acc tac ctt gca tct	1160
Leu Asp Leu Met Met Asn Val Asn Thr Arg Gly Thr Tyr Leu Ala Ser	
120 125 130	
aaa gca tgt att cct tat ttg aaa aag agc aaa gtt gct cat atc ctc	1208
Lys Ala Cys Ile Pro Tyr Leu Lys Lys Ser Lys Val Ala His Ile Leu	
135 140 145	
aat atc agt cca cca ctg aac cta aat cca gtt tgg ttc aaa cag cac	1256
Asn Ile Ser Pro Pro Leu Asn Leu Asn Pro Val Trp Phe Lys Gln His	
150 155 160 165	
tgt gct tat acc att gct aag tat ggt atg tct atg tat gtg ctt gga	1304
Cys Ala Tyr Thr Ile Ala Lys Tyr Gly Met Ser Met Tyr Val Leu Gly	
170 175 180	
atg gca gaa gaa ttt aaa ggt gaa att gca gtc aat gca tta tgg cct	1352
Met Ala Glu Glu Phe Lys Gly Glu Ile Ala Val Asn Ala Leu Trp Pro	
185 190 195	
aaa aca gcc ata cac act gct gct atg gat atg ctg gga gga cct ggt	1400
Lys Thr Ala Ile His Thr Ala Ala Met Asp Met Leu Gly Gly Pro Gly	
200 205 210	
atc gaa agc cag tgt aga aaa gtt gat atc att gca gat gca gca tat	1448
Ile Glu Ser Gln Cys Arg Lys Val Asp Ile Ile Ala Asp Ala Ala Tyr	
215 220 225	
tcc att ttc caa aag cca aaa agt ttt act ggc aac ttt gtc att gat	1496
Ser Ile Phe Gln Lys Pro Lys Ser Phe Thr Gly Asn Phe Val Ile Asp	
230 235 240 245	
gaa aat atc tta aaa gaa gaa gga ata gaa aat ttt gac gtt tat gca	1544
Glu Asn Ile Leu Lys Glu Glu Gly Ile Glu Asn Phe Asp Val Tyr Ala	
250 255 260	
att aaa cca ggt cat cct ttg caa cca gat ttc ttc tta gat gaa tac	1592
Ile Lys Pro Gly His Pro Leu Gln Pro Asp Phe Phe Leu Asp Glu Tyr	
265 270 275	
cca gaa gca gtt agc aag aaa gtg gaa tca act ggt gct gtt cca gaa	1640

Pro	Glu	Ala	Val	Ser	Lys	Lys	Val	Glu	Ser	Thr	Gly	Ala	Val	Pro	Glu		
		280					285					290					
ttc	aaa	gaa	gag	aaa	ctg	cag	ctg	caa	cca	aaa	cca	cgt	tct	gga	gct	1688	
Phe	Lys	Glu	Glu	Lys	Leu	Gln	Leu	Gln	Pro	Lys	Pro	Arg	Ser	Gly	Ala		
	295					300					305						
gtg	gaa	gaa	aca	ttt	aga	att	gtt	aag	gac	tct	ctc	agt	gat	gat	gtt	1736	
Val	Glu	Glu	Thr	Phe	Arg	Ile	Val	Lys	Asp	Ser	Leu	Ser	Asp	Asp	Val		
	310				315					320					325		
gtt	aaa	gcc	act	caa	gca	atc	tat	ctg	ttt	gaa	ctc	tcc	ggg	gaa	gat	1784	
Val	Lys	Ala	Thr	Gln	Ala	Ile	Tyr	Leu	Phe	Glu	Leu	Ser	Gly	Glu	Asp		
				330					335						340		
ggg	ggc	acg	tgg	ttt	ctt	gat	ctg	aaa	agc	aag	ggg	ggg	aat	gtc	gga	1832	
Gly	Gly	Thr	Trp	Phe	Leu	Asp	Leu	Lys	Ser	Lys	Gly	Gly	Asn	Val	Gly		
			345					350					355				
tat	gga	gag	cct	tct	gat	cag	gca	gat	gtg	gtg	atg	agt	atg	act	act	1880	
Tyr	Gly	Glu	Pro	Ser	Asp	Gln	Ala	Asp	Val	Val	Met	Ser	Met	Thr	Thr		
		360					365						370				
gat	gac	ttt	gta	aaa	atg	ttt	tca	ggg	aaa	cta	aaa	cca	aca	atg	gca	1928	
Asp	Asp	Phe	Val	Lys	Met	Phe	Ser	Gly	Lys	Leu	Lys	Pro	Thr	Met	Ala		
		375				380					385						
ttc	atg	tca	ggg	aaa	ttg	aag	att	aaa	ggg	aac	atg	gcc	cta	gca	atc	1976	
Phe	Met	Ser	Gly	Lys	Leu	Lys	Ile	Lys	Gly	Asn	Met	Ala	Leu	Ala	Ile		
	390				395					400					405		
aaa	ttg	gag	aag	cta	atg	aat	cag	atg	aat	gcc	aga	ctg	tga			2018	
Lys	Leu	Glu	Lys	Leu	Met	Asn	Gln	Met	Asn	Ala	Arg	Leu	*				
				410					415								
aggaaaaatat	aaaaaaaaaag	tcgactgcta	tgctcaaaaa	gtaaaaaaag	ctcaacagtt	2078											
aaaatctaata	gtttgttttc	tttctgttta	tattataagg	atatgcacgt	ttgttctgga	2138											
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ccctttgagc	cttacatctc	attcactgtc	tttctccaag	aaaagtattt	tgggcggaca	2318											
gtcagatcaa	gcagtaaaat	tagctctttc	aaatcttctt	gtcatgtaaa	atgaagctag	2378											
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wtttttatat	acytawtttw	aarraawyy	twwwwrkwc	mtttttwmcaa	aaawtwttta	2498											
aaawkrwww	kwrytskgs	mgraswmwaw	rwrmm			2535											

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 <212> PRT
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 Gly Ile Gly Gln Ala Ala Ala Leu Ala Phe Ala Arg Glu Gly Ala Lys
 20 25 30
 Val Ile Ala Thr Asp Ile Asn Glu Ser Lys Leu Gln Glu Leu Glu Lys
 35 40 45

Tyr	Pro	Gly	Ile	Gln	Thr	Arg	Val	Leu	Asp	Val	Thr	Lys	Lys	Lys	Gln
50						55					60				
Ile	Asp	Gln	Phe	Ala	Asn	Glu	Val	Glu	Arg	Leu	Asp	Val	Leu	Phe	Asn
65					70					75					80
Val	Ala	Gly	Phe	Val	His	His	Gly	Thr	Val	Leu	Asp	Cys	Glu	Glu	Lys
				85					90					95	
Asp	Trp	Asp	Phe	Ser	Met	Asn	Leu	Asn	Val	Arg	Ser	Met	Tyr	Leu	Met
			100					105					110		
Ile	Lys	Ala	Phe	Leu	Pro	Lys	Met	Leu	Ala	Gln	Lys	Ser	Gly	Asn	Ile
		115					120					125			
Ile	Asn	Met	Ser	Ser	Val	Ala	Ser	Ser	Val	Lys	Gly	Val	Val	Asn	Arg
	130					135					140				
Cys	Val	Tyr	Ser	Thr	Thr	Lys	Ala	Ala	Val	Ile	Gly	Leu	Thr	Lys	Ser
145					150					155					160
Val	Ala	Ala	Asp	Phe	Ile	Gln	Gln	Gly	Ile	Arg	Cys	Asn	Cys	Val	Cys
				165				170						175	
Pro	Gly	Thr	Val	Asp	Thr	Pro	Ser	Leu	Gln	Glu	Arg	Ile	Gln	Ala	Arg
			180					185					190		
Gly	Asn	Pro	Glu	Glu	Ala	Arg	Asn	Asp	Phe	Leu	Lys	Arg	Gln	Lys	Thr
		195					200					205			
Gly	Arg	Phe	Ala	Thr	Ala	Glu	Glu	Ile	Ala	Met	Leu	Cys	Val	Tyr	Leu
	210					215					220				
Ala	Ser	Asp	Glu	Ser	Ala	Tyr	Val	Thr	Gly	Asn	Pro	Val	Ile	Ile	Asp
225					230					235					240
Gly	Gly	Trp	Ser	Leu											
				245											

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ggggccgccg	ccctacctga	ggccgccatc	cacgccggtt	gagtcgcgtt	ctgccgcctc					180
ccgcctgttg	tgctcctga	actgcgtccg	ccgtytaggt	aagtttaaag	ctcaggtcga					240
gaccgggcct	ttgtccggcg	ctcccttgga	gcctacctag	actcagccgg	ctctccacgc					300
tttgctgac	cctgcttgct	caactctacg	tctttgtttc	gttttctggt	ctgcgccgtt					360
acagatccaa	gctctgaaaa	accagaaagt	taactggtaa	gtttagtctt	tttgtctttt					420
atttcaggtc	ccggatccgg	tggtggtgca	aatcaaagaa	ctgctcctca	gtggatgttg					480
cctttacttc	taggcctgta	cggaagtgtt	acttctgctc	taaaagctgc	ggaattctaa					540
tacgactcac	tatagggagt	cgaccacgc	gtccgcaaac	cgagttctgg	agaacgccat					600
cagctcgctg	cttaaaatta	aaccacaggt	tccatt atg	ggt cga ctt gat ggg						654
			Met	Gly Arg Leu Asp Gly						

	1	5	
aaa gtc atc atc ctg acg gcc gct gct cag ggg att ggc caa gca gct Lys Val Ile Ile Leu Thr Ala Ala Ala Gln Gly Ile Gly Gln Ala Ala	10	20	702
gcc tta gct ttt gca aga gaa ggt gcc aaa gtc ata gcc aca gac att Ala Leu Ala Phe Ala Arg Glu Gly Ala Lys Val Ile Ala Thr Asp Ile	25	35	750
aat gag tcc aaa ctt cag gaa ctg gaa aag tac ccg ggt att caa act Asn Glu Ser Lys Leu Gln Glu Leu Glu Lys Tyr Pro Gly Ile Gln Thr	40	50	798
cggt gtc ctt gat gtc aca aag aag aaa caa att gat cag ttt gcc aat Arg Val Leu Asp Val Thr Lys Lys Lys Gln Ile Asp Gln Phe Ala Asn	55	65	846
gaa gtt gag aga ctt gat gtt ctc ttt aat gtt gct ggt ttt gtc cat Glu Val Glu Arg Leu Asp Val Leu Phe Asn Val Ala Gly Phe Val His	75	80	894
cat gga act gtc ctg gat tgt gag gag aaa gac tgg gac ttc tcg atg His Gly Thr Val Leu Asp Cys Glu Glu Lys Asp Trp Asp Phe Ser Met	90	95	942
aat ctc aat gtg cgc agc atg tac ctg atg atc aag gca ttc ctt cct Asn Leu Asn Val Arg Ser Met Tyr Leu Met Ile Lys Ala Phe Leu Pro	105	110	990
aaa atg ctt gct cag aaa tct ggc aat att atc aac atg tct tct gtg Lys Met Leu Ala Gln Lys Ser Gly Asn Ile Ile Asn Met Ser Ser Val	120	125	1038
gct tcc agc gtc aaa gga gtt gtg aac aga tgt gtg tac agc aca acc Ala Ser Ser Val Lys Gly Val Val Asn Arg Cys Val Tyr Ser Thr Thr	135	140	1086
aag gca gcc gtg att ggc ctc aca aaa tct gtg gct gca gat ttc atc Lys Ala Ala Val Ile Gly Leu Thr Lys Ser Val Ala Ala Asp Phe Ile	155	160	1134
cag cag ggc atc agg tgc aac tgt gtg tgc cca gga aca gtt gat acg Gln Gln Gly Ile Arg Cys Asn Cys Val Cys Pro Gly Thr Val Asp Thr	170	175	1182
cca tct cta caa gaa aga ata caa gcc aga gga aat cct gaa gag gca Pro Ser Leu Gln Glu Arg Ile Gln Ala Arg Gly Asn Pro Glu Glu Ala	185	190	1230
cggt aat gat ttc ctg aag aga caa aag acg gga aga ttc gca act gca Arg Asn Asp Phe Leu Lys Arg Gln Lys Thr Gly Arg Phe Ala Thr Ala	200	205	1278
gaa gaa ata gcc atg ctc tgc gtg tat ttg gct tct gat gaa tct gct Glu Glu Ile Ala Met Leu Cys Val Tyr Leu Ala Ser Asp Glu Ser Ala	215	220	1326

tat gta act ggt aac cct gtc atc att gat gga ggc tgg agc ttg tga	1374
Tyr Val Thr Gly Asn Pro Val Ile Ile Asp Gly Gly Trp Ser Leu *	
235 240 245	

ttttaggatc tccatggtgg gaaggaaggc aggcccttcc tatccacagt gaacctgggt	1434
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acataaaatg aatgcmattg ttgktggtaa cttgttattg ca	1716